

TABLE 1: Included Genes

## Lysine biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
5	6	RXA00657				AMINOACID BIOSYNTHESIS REGULATOR
7	8	RXA02229	GR00653	2793	3617	DIAMINOPELMATE EPIMERASE (EC 5.1.1.7)
9	10	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
11	12	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
13	14	RXC02390				MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
15	16	RXC01796				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
17	18	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
19	20	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
21	22	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

## Lysine biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
25	26	RXA00533	GR00137	3469	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
27	28	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
29	30	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPELMATE DESUCCINYLASE (EC 3.5.1.18)
31	32	RXA00044	GR00007	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
33	34	RXA00863	GR00236	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
35	36	RXA00864	GR00236	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum
37	38	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
39	40	RXN00355	VV0135	31980	30961	MESO-DIAMINOPELMATE D-DEHYDROGENASE
41	42	F RXA00352	GR00068	861	4	MESO-DIAMINOPELMATE D-DEHYDROGENASE (EC 1.4.1.16)
43	44	RXA00972	GR00274	3	1379	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
45	46	RXA02653	GR00752	5237	7234	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
49	50	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
51	52	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
53	54	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
55	56	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
57	58	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
59	60	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
61	62	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
65	66	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
67	68	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

### Metabolism of methionine and S-adenosyl methionine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	metZ or met				O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10)
3	4	metC				Cystathionine-γ-lyase
69	70	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
71	72	RXN00403	VV00086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
73	74	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
75	76	RXS03158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
77	78	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
79	80	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
81	82	RXS03159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
83	84	F RXA02768	GR00770	1919	2521	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
85	86	RXA00216	GR00032	16286	15297	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
87	94	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
89	90	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
91	91	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
93	94	RXN03074	VV0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAUQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

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<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
95	96	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-)
97	98	RXN00132	WV0124	3612	5045	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 3.3.1.1)
99	100	F RXA00132	GR00020	7728	7624	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 3.3.1.1)
101	102	F RXA01371	GR00398	2339	3634	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 3.3.1.1)
103	104	RXN02085				ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.14)
105	106	F RXA02085	GR00629	3496	5295	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.14)
107	108	F RXA02086	GR00629	5252	5731	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.14)
109	110	RXN02648				ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.14)
111	112	F RXA02648	GR00751	5254	4730	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.14)
113	114	F RXA02658	GR00752	14764	15447	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.14)
115	116	RXC02238				ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.14)
117	118	RXC00128				ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.14)

## S-2adenosyl methionine (SAM) Biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
119	120	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

### TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkf	transketolase	
AB024708	glfB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	
AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY; glnB; glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroeductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroeductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95



GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohana, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
L35906	dtxr	Diphtheria toxin repressor	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M13774		Prephenate dehydratase	Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16175	5S rRNA		Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rosol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranyl phosphate transferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIR; clgIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cgIIIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thiR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock A TP-binding protein	
U53587	aphA-3	3'5"-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the <i>dapA</i> gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69103	csp2	Surface layer protein PS2	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X69104		IS3 related insertion element	
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75083, X70584	mtrA	5-methyltryptophan resistance	
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X78491	aceB	Malate synthase	Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X80629	16S rDNA	16S ribosomal RNA	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X82061	16S rDNA	16S ribosomal RNA	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
			Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from C. glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE, lysG	Lysine exporter protein; Lysine export regulator protein	Vrtiljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)
X96580	panB; panC; xylB	3-methyl-2-oxobutanate hydroxymethyltransferase; pantoate-beta-	Sahm, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate

GenBank™ Accession No.	Gene Name	alanine ligase; xylulokinase Gene Function	overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999) Reference
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	mutC; ftsQ/divD; ftsZ	UPD-N-acetylmutamate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynebacterium 304L	Moreau, S. et al. "Analysis of the integration functions of $\phi$ phi304L: An inte-grase module among coryne-phages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							



Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ	Other origin
Corynebacterium	glutamicum			B12418						
Corynebacterium	glutamicum			B11476						
Corynebacterium	glutamicum	21608								
Corynebacterium	lilium		P973							
Corynebacterium	nitrilophilus	21419				11594				
Corynebacterium	spec.		P4445							
Corynebacterium	spec.		P4446							
Corynebacterium	spec.	31088								
Corynebacterium	spec.	31089								
Corynebacterium	spec.	31090								
Corynebacterium	spec.	31090								
Corynebacterium	spec.	31090								
Corynebacterium	spec.	15954							20145	
Corynebacterium	spec.	21857								
Corynebacterium	spec.	21862								
Corynebacterium	spec.	21863								
Corynebacterium	Glutamicum*									ASO19
Corynebacterium	Glutamicum**									ASO19 E12
Corynebacterium	Glutamicum***									HL457
Corynebacterium	Glutamicum****									HL459

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4<sup>th</sup> edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

\* Spontaneous rifampin-resistant mutant of *C. glutamicum* ATCC13059<sup>d</sup> Yoshihama *et al.*, 1985

\*\* Restriction-deficient variant of ASO19 Follett *et al.*, 1993

\*\*\* *metC*-disrupted mutant of ASO19E12 This study

\*\*\*\* *metC*-disrupted mutant of ASO19E12 This study

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx000657	906	GB_BA1:AF064700	3481	AF064700	Rhodococcus sp	Rhodococcus sp	40,265	15-Jul-98
metc	1314	GB_BA2:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome, segment 143/162	Mycobacterium tuberculosis	61,278	23-Jun-99
metc	978	GB_BA2:CORCSLYS	2821	M89831	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake	Corynebacterium glutamicum	99,591	04-JUN-1998
rx000023	3579	GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	clER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	clER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
rx000044	1059	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	42,979	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	42,979	07-OCT-1996
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	17-DEC-1993
rx000064	1401	GB_PAT:E16763	2517	E16763	gDNA encoding aspartate transferase (AAT).	Corynebacterium glutamicum	95,429	28-Jul-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98	Drosophila melanogaster	31,111	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	31,111	2-Aug-99
rx000072		GB_HTG2:AC007892	134257	AC007892	***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98	Drosophila melanogaster	31,111	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rx000105	798	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,753	17-Jun-98
		GB_BA1:ECU29581	71128	U29581	Escherichia coli K-12 genome; approximately 63 to 64 minutes.	Escherichia coli	35,669	14-Jan-97
		GB_BA2:AE000366	10405	AE000366	Escherichia coli K-12 MG1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
rx000106	579	GB_EST15:AA494237	367	AA494237	ng83f04.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941407 similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE ;, mRNA sequence.	Homo sapiens	42,896	20-Aug-97
		GB_BA2:AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds.	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT:AR041189	654	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-99
rx000115	1170	GB_PR4:AC007110	148336	AC007110	Homo sapiens chromosome 17, clone hRPK.472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR-1999
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS *** , 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS *** , 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99



## TABLE 4: ALIGNMENT RESULTS

[illegible]

## TABLE 4: ALIGNMENT RESULTS

rx00198	672	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	92,113	13-MAR-1999
		GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	93,702	13-MAR-1999
		GB_EST24:AI232702	528	AI232702	EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence.	Rattus sp	34,221	31-Jan-99
rx00216	1113	GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
		GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
		GB_PR2:CNS01DSA	159400	AL121766	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPC1-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	38,796	11-Nov-99
rx00219	1065	GB_HTG2:AC005079_0	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
rx00223	1212	GB_BA1:PPEA3NIF	19771	X99694	Plasmid pEA3 nitrogen fixation genes.	Enterobacter agglomerans	48,826	2-Aug-96
		GB_BA2:AF128444	2477	AF128444	Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence.	Rhodobacter capsulatus	40,135	22-MAR-1999
		GB_HTG4:AC010111	138938	AC010111	Drosophila melanogaster chromosome 3L70C1 clone RPC198-9B18, *** SEQUENCING IN PROGRESS *** 64 unordered pieces.	Drosophila melanogaster	39,527	16-OCT-1999
rx00229	803	GB_BA2:AF124518	1758	AF124518	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	Corynebacterium glutamicum	98,237	18-MAY-1999
		GB_PR3:AC004593	150221	AC004593	Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.	Homo sapiens	36,616	18-Apr-98
		GB_HTG2:AC006907	188972	AC006907	Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS *** 25 unordered pieces.	Caenorhabditis elegans	37,095	26-Feb-99
rx00241	1626	GB_BA1:CGLYSI	4232	X60312	C-glutamicum lysyl gene for L-lysine permease.	Corynebacterium glutamicum	100,000	30-Jan-92
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
rx00262	1197	GB_IN2:EHU89655	3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	36,496	23-MAY-1997
		GB_IN2:EHU89655	3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	37,544	23-MAY-1997
rx00266	531	GB_RO:AF016190	2939	AF016190	Mus musculus connexin-36 (Cx36) gene, complete cds.	Mus musculus	41,856	9-Feb-99
		EM_PAT:E09719	3505	E09719	DNA encoding precursor protein of alkaline cellulase.	Bacillus sp.	34,741	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:E02133	3494	E02133	gDNA encoding alkaline cellulase.	Bacillus sp.	34,741	29-Sep-97
		GB_IN1:CEI1K05F6	36912	AF040653	Caenorhabditis elegans cosmid K05F6	Caenorhabditis elegans	36,943	6-Jan-98

**TABLE 4: ALIGNMENT RESULTS**

GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	36,658	9-Apr-97
GB_RO:RNU30789	3510	U30789	Rattus norvegicus clone N27 mRNA.	Rattus norvegicus	38,190	20-Aug-96
GB_BA2:CGU31281	1614	U31281	Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds.	Corynebacterium glutamicum	99,111	21-Nov-96
GB_BA1:BRLBIOBA	1647	D14084	Brevibacterium flavum gene for biotin synthetase, complete cds.	Corynebacterium glutamicum	98,489	3-Feb-99
GB_PAT:E03937	1005	E03937	DNA sequence encoding Brevibacterium flavum biotin-synthase.	Corynebacterium glutamicum	98,207	29-Sep-97
GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	35,615	24-Jun-99
GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	60,917	15-Jun-96
GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	44,606	24-Jun-99
GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	52,516	15-Jun-96
GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,079	24-Jun-99
GB_OM:BOVELA	3242	J02717	Bovine elastin a mRNA, complete cds.	Bos taurus	39,351	27-Apr-93
GB_BA1:CGTHRC	3120	X56037	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).	Corynebacterium glutamicum	99,808	17-Jun-97
GB_PAT:I09078	3146	I09078	Sequence 4 from Patent WO 8809819.	Unknown.	99,617	02-DEC-1994
GB_BA1:BLTHRESYN	1892	Z29563	Brevibacterium lactofermentum; ATCC 13869; DNA (genomic);.	Corynebacterium glutamicum	99,170	20-Sep-95
GB_BA1:CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene.	Corynebacterium glutamicum	100,000	28-Aug-97
GB_BA2:AF005635	1690	AF005635	Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds.	Corynebacterium glutamicum	98,906	14-Jun-99
GB_BA1:MSGB27CS	38793	L78817	Mycobacterium leprae cosmid B27 DNA sequence.	Mycobacterium leprae	66,345	15-Jun-96
GB_EST27:AI455217	624	AI455217	LD21828.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828 3prime, mRNA sequence.	Drosophila melanogaster	34,510	09-MAR-1999
GB_BA2:SSU30252	2891	U30252	Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site 1 for vector use.	Synechococcus PCC7942	37,084	29-OCT-1999
GB_EST21:AA911262	581	AA911262	oe75a02 s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417418 3' similar to gb:A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN);, mRNA sequence.	Homo sapiens	37,500	21-Apr-98
GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	52,972	09-MAR-1995
GB_IN2:AC004373	72722	AC004373	Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.	Drosophila melanogaster	46,341	17-Jul-98
GB_IN2:AF145653	3197	AF145653	Drosophila melanogaster clone GH08860 BcDNA.GH08860 (BcDNA.GH08860) mRNA, complete cds.	Drosophila melanogaster	49,471	14-Jun-99
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds	Corynebacterium glutamicum	96,556	13-MAR-1999
GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	39,496	17-Jun-98
GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,946	16-Aug-99
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,374	13-MAR-1999
GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	41,333	17-Jun-98
GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,554	16-Aug-99

**TABLE 4: ALIGNMENT RESULTS**

rx00367	4653	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,312	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	36,971	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,905	16-Aug-99
rx00371	1917	GB_VI:SBVORFS	7568	M89923	Sugarcane bacilliform virus ORF 1,2, and 3 DNA, complete cds.	Sugarcane bacilliform virus	35,843	12-Jun-93
		GB_EST37:AI967505	380	AI967505	Ljirpest03-215-c10 Ljirmp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence.	Lotus japonicus	42,593	24-Aug-99
rx00377	1245	GB_IN1:CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9.	Caenorhabditis elegans	34,295	22-Jan-98
		GB_BA1:CCU13664	1678	U13664	Caulobacter crescentus uroporphyrinogen decarboxylase homolog (hemE) gene, partial cds.	Caulobacter crescentus	36,832	24-MAR-1995
		GB_PL1:ANSDGENE	1299	Y08866	A.nidulans sD gene.	Emericella nidulans	39,603	17-OCT-1996
		GB_GSS4:AQ730303	483	AQ730303	HS_5505_B1_C04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=7 Row=F, genomic survey sequence.	Homo sapiens	36,728	15-Jul-99
rx00382	1425	GB_BA1:PAHEML	4444	X82072	P.aeruginosa hemL gene.	Pseudomonas aeruginosa	54,175	18-DEC-1995
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	61,143	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	61,143	03-DEC-1996
rx00383	1467	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	43,981	27-Aug-99
		GB_HTG2:AC006269	167171	AC006269	Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	35,444	10-Jun-99
		GB_HTG2:AC007638	178053	AC007638	Homo sapiens chromosome 17 clone hRPK.515_O_17 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	34,821	22-MAY-1999
rx00391	843	GB_EST38:AW017053	613	AW017053	EST727398 Schistosoma mansoni male, Phil LoVerde/Joel Merrick	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT:AR065852	32207	AR065852	Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence. Sequence 20 from patent US 5849564.	Unknown.	38,586	29-Sep-99
		GB_VI:AF148805	28559	AF148805	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds.	Kaposi's sarcoma-associated herpesvirus	38,509	2-Aug-99
rx00393	1017	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,308	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	39,282	03-DEC-1996
		GB_BA1:MLB1306	7762	Y13803	Mycobacterium leprae cosmid B1306 DNA.	Mycobacterium leprae	39,228	24-Jun-97
rx00402	623	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,672	19-MAR-1998
		GB_BA2:AF109162	4514	AF109162	Corynebacterium diphtheriae heme uptake locus, complete sequence.	Corynebacterium diphtheriae	40,830	8-Jun-99
		GB_BA2:AF092918	20758	AF092918	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	50,161	06-DEC-1998
rx00403	1254	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,920	19-MAR-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	52,898	23-Jun-99
		GB_EST23:AI111288	750	AI111288	SWOVAMICAQ02A05SK Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SWOVAMCAQ02A05 5', mRNA sequence.	Onchocerca volvulus	37,565	31-Aug-98

**TABLE 4: ALIGNMENT RESULTS**

rx00405	613	GB_BA1:MTV016 GB_PR4:AC005145	53662 143678	AL021841 AC005145	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Homo sapiens Xp22-166-169 GSHB-523A23 (Genome Systems Human BAC library) complete sequence.	Mycobacterium tuberculosis Homo sapiens	57,259 34,179	23-Jun-99 08-DEC-1998
rx00420	1587	GB_BA1:MTV016 GB_BA1:MTY13D12 GB_BA1:MSGY126 GB_BA1:MSG971CS GB_BA1:AFACBBTZ	53662 37085 37164 37566 2760	AL021841 Z80343 AD000012 L78821 M68904	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Mycobacterium tuberculosis H37Rv complete genome; segment 156/162. Mycobacterium tuberculosis sequence from clone y126. Mycobacterium leprae cosmid B971 DNA sequence. Alcaligenes eutrophus chromosomal transketolase (cbbTc) and phosphoglycolate phosphatase (cbbZc) genes, complete cds.	Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Ralstonia eutropha	40,169 62,031 61,902 39,651 38,677	23-Jun-99 17-Jun-98 10-DEC-1996 15-Jun-96 27-Jul-94
rx00435	1296	GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
rx00437	579	GB_HTG4:AC009541 GB_PR4:AC005951	169583 155450	AC009541 AC005951	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens Homo sapiens	36,335 31,738	12-OCT-1999 18-Nov-98
rx00439	591	GB_BA1:MTV016 GB_PL2:AF167358 GB_HTG3:AC009120	53662 1022 269445	AL021841 AF167358 AC009120	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Rumex acetosa expansin (EXP3) gene, partial cds. Homo sapiens chromosome 16 clone RPCI-11_484E3, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces.	Mycobacterium tuberculosis Rumex acetosa Homo sapiens	37,088 46,538 43,276	23-Jun-99 17-Aug-99 3-Aug-99
rx00440	582	GB_BA2:SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	43,080	27-OCT-1999
rx00441	1287	GB_BA1:SC2E1 GB_BA1:SC2E1 GB_PR2:HS173D1	38962 38962 117338	AL023797 AL023797 AL031984	Streptomyces coelicolor cosmid 2E1. Streptomyces coelicolor cosmid 2E1. Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33. Contains ESTs, STSs and GSSs, complete sequence.	Streptomyces coelicolor Streptomyces coelicolor Homo sapiens	42,931 36,702 38,027	4-Jun-98 4-Jun-98 23-Nov-99
rx00446	987	GB_HTG2:HSDJ719K3 GB_HTG2:HSDJ719K3 GB_HTG4:AC009367 GB_HTG4:AC009367	267114 267114 226055 226055	AL109931 AL109931 AC009367 AC009367	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Streptomyces coelicolor cosmid D78. Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces. Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Homo sapiens Homo sapiens Streptomyces coelicolor Drosophila melanogaster Drosophila melanogaster	34,521 34,521 56,410 34,959 34,959	03-DEC-1999 03-DEC-1999 26-Nov-98 16-OCT-1999 16-OCT-1999
rx00448	1143	GB_PR3:AC003670 GB_HTG2:AF029367 GB_HTG2:AF029367	88945 148676 148676	AC003670 AF029367 AF029367	Homo sapiens 12q13.1 PAC RPCI1-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence. Homo sapiens chromosome 12 clone RPCI-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces. Homo sapiens chromosome 12 clone RPCI-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces.	Homo sapiens Homo sapiens Homo sapiens	35,682 31,373 31,373	9-Jun-98 18-OCT-1997 18-OCT-1997

TABLE 4: ALIGNMENT RESULTS

rx00450	424	GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_EST35:A1818057	412	A1818057	wk14a08.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412278 3' similar to gb:Y00764 UBQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	35,714	24-Aug-99
rx00461	975	GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	39,308	8-Aug-97
		GB_IN1:DMC85E4	29352	AL021086	Drosophila melanogaster cosmid clone 86E4.	Drosophila melanogaster	37,487	27-Apr-99
rx00465		GB_GSS15:AQ640325	467	AQ640325	927P1-2H3.TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence.	Trypanosoma brucei	38,116	8-Jul-99
rx00487	1692	GB_BA1:BAGUAA	3866	Y10499	B.ammoniaenes guaA gene.	Corynebacterium ammoniaenes	74,259	8-Jan-98
rx00488	1641	GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	37,248	01-MAR-1994
		GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome, segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
		GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,451	17-Jun-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	39,178	01-MAR-1994
rx00489	1245	GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiI and whiK loci.	Streptomyces coelicolor	60,835	17-Sep-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	38,041	01-MAR-1994
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
rx00533	1155	GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
		GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11)	Corynebacterium glutamicum	99,913	17-Feb-97
		GB_BA1:CGCYSCASD	1591	X82928	C.glutamicum aspartate-semialdehyde dehydrogenase gene.	Corynebacterium glutamicum	99,221	17-Feb-97
rx00534	1386	GB_PAT:A07546	2112	A07546	Recombinant DNA fragment (PstI-XhoI).	synthetic construct	99,391	30-Jul-93
		GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,856	17-Feb-97
		GB_BA1:CORASKD	2957	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds.	Corynebacterium flavesens	98,701	11-Jun-93
rx00536	1494	GB_PAT:E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.	Corynebacterium glutamicum	98,773	28-Jul-99
		GB_BA1:CGLEUA	3492	X70959	C.glutamicum gene leuA for isopropylmalate synthase.	Corynebacterium glutamicum	100,000	10-Feb-99
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	68,003	24-Jun-99
		GB_BA1:MTU88526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.	Mycobacterium tuberculosis	68,185	26-Feb-97

**TABLE 4: ALIGNMENT RESULTS**

rx00537	2409	GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	63,187	21-Sep-99
		GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	62,401	17-Jun-98
		GB_BA1:MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (purL) gene, complete cds.	Mycobacterium tuberculosis	62,205	28-Jan-97
rx00541	792	GB_PAT:I92052	2115	I92052	Sequence 19 from patent US 5726299.	Unknown.	98,359	01-DEC-1998
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	62,468	24-Jun-97
		GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	60,814	17-Jun-98
rx00558	1470	GB_BA1:BAPURF	1885	X91252	B.ammoniaenes purF gene	Corynebacterium ammoniagenes	66,095	5-Jun-97
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	64,315	09-MAR-1995
		GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	64,863	17-Jun-98
rx00579	1983	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740	Unknown.	98,810	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	98,810	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	98,810	24-Jun-98
rx00580	1425	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	99,368	24-Jun-98
		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	99,368	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	99,368	08-OCT-1997 (Rel. 52, Created)
rx00581	1092	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	24-Jun-98
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created)
rx00584	1248	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	05-DEC-1998
		GB_BA1:CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,236	26-Apr-93
		GB_BA1:AOPCZA361	37941	AJ223998	Amycolatopsis orientalis cosmid PCZA361.	Amycolatopsis orientalis	54,553	29-MAR-1999
		GB_BA1:D90714	14358	D90714	Escherichia coli genomic DNA. (16.8 - 17.1 min).	Escherichia coli	53,312	7-Feb-99
rx00618	1230	GB_EST19:AA802737	280	AA802737	GM06236.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06236 5prime, mRNA sequence.	Drosophila melanogaster	39,928	25-Nov-98
		GB_EST28:A1534381	581	A1534381	SD07186.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858; Ani FBgn0011558 PID:g927407 SPTREMBL.Q24240, mRNA sequence.	Drosophila melanogaster	41,136	18-MAR-1999
rx00619	1551	GB_IN1:DMANILLIN	4029	X89858	D.melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	8-Nov-95
		GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	62,776	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	61,831	24-Jun-97
		GB_PAT:A60305	1845	A60305	Sequence 5 from Patent WO9708323.	unidentified	61,785	06-MAR-1998
rx00620	1014	GB_PL2:AF063247	1450	AF063247	Pneumocystis carinii f. sp. ratti enolase mRNA, complete cds.	Pneumocystis carinii f. sp. ratti	41,060	5-Jan-99
		GB_BA1:STMAPP	2069	M91546	Streptomyces lividans aminopeptidase P (PepP) gene, complete cds.	Streptomyces lividans	37,126	12-Jun-93

TABLE 4: ALIGNMENT RESULTS

rx00624	810	GB_HTG3:AC008763	214575	AC008763	Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***; 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
rx00626	1386	GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	36,986	2-Sep-99
		GB_EST13:AA362167	372	AA362167	EST71561 Macrophage I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378	21-Apr-97
		GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694	2-Sep-99
		GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv, complete genome; segment 36/162.	Mycobacterium tuberculosis	57,971	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,806	24-Jun-97
rx00632	795	GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	38,007	09-MAR-1995
		GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358	3-Feb-99
rx00633	1392	GB_PAT:E04041	675	E04041	DNA sequence coding for dethiobiotin synthetase.	Corynebacterium glutamicum	98,074	29-Sep-97
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	93,814	29-Sep-97
		GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690	3-Feb-99
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755	29-Sep-97
rx00688	666	GB_BA2:EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds.	Erwinia herbicola	55,564	4-Nov-96
		GB_BA1:MTV041	28826	AL021958	Mycobacterium tuberculosis H37Rv complete genome; segment 35/162.	Mycobacterium tuberculosis	60,030	17-Jun-98
		GB_BA1:BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds).	Corynebacterium glutamicum	99,563	3-Feb-99
rx00708	930	GB_BA2:MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030	27-Jan-99
		GB_BA2:AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116	5-Jul-99
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419	21-MAY-1993
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	47,419	29-Sep-97
		GB_PAT:I78753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
rx00717	1083	GB_PAT:I92042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	55,228	17-Jun-98
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300	17-Jun-98
		GB_GSS12:AQ420755	671	AQ420755	RPCI-11-168G18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-168G18, genomic survey sequence.	Homo sapiens	35,750	23-MAR-1999
rx00727	1035	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99
rx00718	831	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	33,888	6-Aug-99
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	33,888	6-Aug-99



**TABLE 4: ALIGNMENT RESULTS**

rx00766	966	GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 Caenorhabditis elegans unordered pieces.	36,737	25-Feb-99
		GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 Caenorhabditis elegans unordered pieces.	36,737	25-Feb-99
rx00770	1293	GB_BA1:D90810	20476	D90810	E.coli genomic DNA, Kohara clone #319(37.4-37.8 min.).	36,526	29-MAY-1997
		GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	66,193	24-Jun-99
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	61,443	09-MAR-1995
		GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	59,938	21-Sep-99
rx00779	1056	GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	64,896	14-OCT-1998
		GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	64,896	14-OCT-1998
		GB_PL2:AF078693	1492	AF078693	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crcys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	57,970	3-Nov-99
rx00780	669	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	54,410	17-Jun-98
		GB_BA1:AVINIFREG	7099	M60090	Azotobacter chroococcum nifU, nifS, nifV, nifP, nifW, nifZ and nifM genes, complete cds.	51,729	26-Apr-93
rx00838	1023	GB_BA2:AF001780	6701	AF001780	Cyanotheca PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds.	36,309	08-MAR-1999
		GB_EST1:Z30506	329	Z30506	ATTS2430 AC16H Arabidopsis thaliana cDNA clone TAI306 3', mRNA sequence.	44,308	11-MAR-1994
		GB_PL2:AC006258	110469	AC006258	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence.	35,571	28-DEC-1998
		GB_EST37:AI998439	455	AI998439	701545695 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence.	36,044	8-Sep-99
rx00863	867	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	99,539	16-Aug-93
		GB_PAT:E16749	2001	E16749	gDNA encoding dihydrodipicolinate synthase (DDPS).	99,539	28-Jul-99
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	99,539	28-Jul-99
rx00864	873	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	99,885	16-Aug-93
		GB_BA1:CGDAPB	1902	X67737	C.glutamicum dapB gene for dihydrodipicolinate reductase.	100,000	1-Apr-93
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	100,000	28-Jul-99
rx00865	1026	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	100,000	16-Aug-93
		GB_PAT:E16752	1411	E16752	gDNA encoding dihydrodipicolinate reductase (DDPR).	99,805	28-Jul-99
		GB_PAT:AF038113	1411	AR038113	Sequence 18 from patent US 5804414.	99,805	29-Sep-99
rx00867	650	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	39,179	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	39,482	22-Aug-97
		GB_BA1:SAU19858	2838	U19858	Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsI) gene, complete cds.	69,706	25-OCT-1996
rx00873	779	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	63,415	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	61,617	29-MAR-1999

## TABLE 4: ALIGNMENT RESULTS

[illegible]

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TABLE 4: ALIGNMENT RESULTS

	GB_GSS1:CNS00RNW 542	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	41,264	28-Jun-99
rx00989 1644	GB_BA1:MTV008 63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 108/162.	40,773	17-Jun-98
	GB_BA1:SCVLSFP 3619	Y13070	S.coelicolor valS, fpgs, ndk genes.	58,119	03-MAR-1998
	GB_BA1:MTV008 63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 108/162.	38,167	17-Jun-98
rx00997 705	GB_BA2:CGU31225 1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxido-reductase (proC) gene, complete cds.	40,841	2-Aug-96
	GB_HTG1:CEY39C12 282838	AL009026	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	36,416	26-OCT-1999
	GB_IN1:CEB0001 39416	Z69634	Caenorhabditis elegans cosmid B0001, complete sequence.	36,416	2-Sep-99
rx01019 1110	GB_HTG2:AC005052 144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	39,172	12-Jun-98
	GB_HTG2:AC005052 144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	39,172	12-Jun-98
	GB_GSS9:QA171808 512	AQ171808	HS_3179_A1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence.	34,661	17-OCT-1998
rx01026 1782	GB_BA1:SC1C2 42210	AL031124	Streptomyces coelicolor cosmid 1C2.	68,275	15-Jan-99
	GB_BA1:ATLEUCD 2982	X84647	A.teichomyceticus leuC and leuD genes.	65,935	04-OCT-1995
rx01027 1131	GB_BA1:MTV012 70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome, segment 132/162.	40,454	23-Jun-99
	GB_BA1:MLCB637 44882	Z99263	Mycobacterium leprae cosmid B637.	38,636	17-Sep-97
	GB_BA1:MTCY349 43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome, segment 131/162.	51,989	17-Jun-98
	GB_BA1:SPUNGMTX 1172	Z21702	S.pneumoniae ung gene and muX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	38,088	15-Jun-94
rx01073 954	GB_BA1:BACOUTB 1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	53,723	26-Apr-93
	GB_PR4:AC007938 167237	AC007938	Homo sapiens clone UWGC-djs201 from 7q31, complete sequence.	34,322	1-Jul-99
	GB_PL2:ATAC006282 92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	36,181	13-MAR-1999
rx01079 2226	GB_BA2:AF112535 4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	99,820	5-Aug-99
	GB_BA1:CANRDFGEN 6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	75,966	18-Apr-98
rx01080 567	GB_BA1:MTV012 70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome, segment 132/162.	38,296	23-Jun-99
	GB_BA2:AF112535 4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	100,000	5-Aug-99
	GB_BA1:CANRDFGEN 6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	65,511	18-Apr-98
rx01087 999	GB_BA1:STNRD 4894	X73226	S.typhimurium nrdEF operon.	52,477	03-MAR-1997
	GB_IN2:AF063412 1093	AF063412	Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds.	43,750	29-MAR-1999
	GB_PR3:HS24M15 134539	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (resistidin), EST.	37,475	23-Nov-99
	GB_IN2:ARU85702 1240	U85702	Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds.	37,319	16-Jul-97

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**TABLE 4: ALIGNMENT RESULTS**

rx01095	857	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	43,243	17-Jun-98
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,471	19-Nov-99
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,836	19-Nov-99
rx01097	477	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	100,000	13-Nov-97
		GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	41,206	13-Nov-97
rx01098	897	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds	Corynebacterium glutamicum	97,933	13-Nov-97
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	40,972	10-DEC-1996
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	61,366	27-Aug-99
rx01100	861	GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	97,154	12-MAR-1998
		GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
		GB_HTG1:HSDJ140A9	221755	AL109917	Homo sapiens chromosome 1 clone RP1-140A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	30,523	23-Nov-99
rx01101	756	GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	94,462	29-Apr-98
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	38,378	23-Jul-99
		GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	60,053	26-Apr-93
rx01104	729	GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds, and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	58,333	26-Apr-93
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	39,045	23-Jul-99
rx01105	1221	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome, segment 70/162.	Mycobacterium tuberculosis	60,364	24-Jun-99
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,931	24-Jun-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	36,851	10-DEC-1996
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	60,902	27-Aug-99
rx01106	1449	GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,233	10-DEC-1996
		GB_BA1:MSHISCD	2298	X65542	M. smegmatis genes hisD and hisC for histidinol dehydrogenase and histidinol-phosphate aminotransferase, respectively.	Mycobacterium smegmatis	60,111	30-Jun-93
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	58,420	24-Jun-99
rx01145	1137	GB_BA1:CORAI	4705	L09232	Corynebacterium glutamicum acetoaldehyde synthase (ilvB) and (ilvN) genes, and acetoaldehyde acid isomeroreductase (ilvC) gene, complete cds.	Corynebacterium glutamicum	100,000	23-Feb-95
		GB_BA1:BRLLVCA	1364	D14551	Brevibacterium flavum ilvC gene for acetoaldehyde acid isomeroreductase, complete cds.	Corynebacterium glutamicum	99,560	3-Feb-99
		GB_PAT.E08232	1017	E08232	DNA encoding acetoaldehyde-acid isomeroreductase.	Corynebacterium glutamicum	99,803	29-Sep-97
rx01162	1449	GB_PAT.A60299	2869	A60299	Sequence 18 from Patent WO9706261.	Aspergillus niger	38,675	06-MAR-1998
		GB_PR3.HS24E5	35506	Z82185	Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.	Homo sapiens	36,204	23-Nov-99

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TABLE 4: ALIGNMENT RESULTS

rxa01208	846	GB_PR3:AC005265	43900	AC005265	Homo sapiens chromosome 19, cosmid F19750, complete sequence.	Homo sapiens	38,363	6-Jul-98
		GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,058	12-Jun-98
					unordered pieces.			
		GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,058	12-Jun-98
					unordered pieces.			
		GB_PL2:TAU55859	2397	U55859	Triticum aestivum heat shock protein 80 mRNA, complete cds.	Triticum aestivum	37,269	1-Feb-99
rxa01209	1528	GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	Homo sapiens	40,000	07-OCT-1999
					IN PROGRESS ***			
		GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	Homo sapiens	40,000	07-OCT-1999
					IN PROGRESS ***			
		GB_PL1:AB010077	77380	AB010077	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence.	Arabidopsis thaliana	36,803	20-Nov-99
rxa01215	1098	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	37,047	17-Jun-98
		GB_IN1:LEIPRP	1887	M76553	Leishmania donovani phosphoribosylpyrophosphate synthetase gene, complete cds.	Leishmania donovani	50,738	7-Jun-93
					complete cds.			
		GB_HTG2:HSJ799D16	130149	AL050344	Homo sapiens chromosome 1 clone RP4-799D16 map p34.3-36.1, *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,135	29-Nov-99
					in unordered pieces.			
rxa01239	2556	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	38,139	17-Jun-98
		GB_PR2:AB029032	6377	AB029032	Homo sapiens mRNA for KIAA1109 protein, partial cds.	Homo sapiens	39,394	4-Aug-99
		GB_GSS9:AAQ107201	355	AQ107201	HS_3098_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3098 Col=5 Row=E, genomic survey sequence.	Homo sapiens	41,408	28-Aug-98
rxa01253	873	GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	Arabidopsis thaliana	36,118	23-DEC-1998
					sequence.			
		GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	Arabidopsis thaliana	35,574	23-DEC-1998
					sequence.			
rxa01321	1044	GB_IN1:CELC06G1	31205	U41014	Caenorhabditis elegans cosmid C06G1.	Caenorhabditis elegans	38,560	30-Nov-95
		GB_GSS14:AQ518843	441	AQ518843	HS_5106_A1_D10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=682 Col=19 Row=G, genomic survey sequence	Homo sapiens	41,121	05-MAY-1999
					Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCI-98	Drosophila melanogaster	40,634	2-Aug-99
		GB_HTG2:AC007473	194859	AC007473	38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***			
					60 unordered pieces.			
		GB_HTG4:AC011696	115847	AC011696	Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCI-98	Drosophila melanogaster	38,290	26-OCT-1999
					35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***			
					108 unordered pieces.			
rxa01352	706	GB_PL2:ATAC005167	83260	AC005167	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	15-OCT-1998
		GB_PL2:ATAC005825	97380	AC005825	Arabidopsis thaliana chromosome II BAC T24121 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
					sequence.			
		GB_HTG3:AC011150	127222	AC011150	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	37,722	01-OCT-1999
rxa01360	259	GB_EST32:A1725583	728	A1725583	BNLGH12371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U86081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,492	11-Jun-99
					Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island. EST.	Homo sapiens	39,738	23-Nov-99

**TABLE 4: ALIGNMENT RESULTS**

rx01361	629	GB_EST34:AV171099	173	AV171099	AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 320002M11, mRNA sequence.	Mus musculus	46,237	6-Jul-99
		GB_RO:AB008915S1	530	AB008915	Mus musculus mGpi1 gene, exon 1.	Mus musculus	45,574	28-Sep-99
		GB_EST22:AI050532	293	AI050532	uc83d10.y1 Sugano mouse kidney mika Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P. ; mRNA sequence.	Mus musculus	44,097	9-Jul-98
rx01361	944	GB_RO:AB008895	3062	AB008895	Mus musculus mRNA for mGpi1p, complete cds.	Mus musculus	41,316	23-Nov-97
		GB_PL1:AB005237	87835	AB005237	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence.	Arabidopsis thaliana	36,606	20-Nov-99
		GB_GSS5:AQ766840	491	AQ766840	HS_2026_A2_C09_TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence.	Homo sapiens	37,916	28-Jul-99
rx01393	993	GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome, segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
		GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	34,831	24-Feb-97
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	35,138	27-Jul-98
		GB_FR3:AC004054	112184	AC004054	Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.	Homo sapiens	37,277	9-Jul-98
rx01394	822	GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
		GB_GSS5:AQ769223	500	AQ769223	HS_3155_B2_G10_TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence.	Homo sapiens	38,400	28-Jul-99
rx01416	630	GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	33,665	24-Feb-97
		GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	62,726	10-Aug-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,159	22-Aug-97
rx01442	1347	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,340	17-Jun-98
		GB_BA1:D90827	18886	D90827	E.coli genomic DNA, Kohara clone #336(41.2-41.6 min.).	Escherichia coli	58,517	21-MAR-1997
		GB_BA1:D90828	14590	D90828	E.coli genomic DNA, Kohara clone #336gap(41.6-41.9 min.).	Escherichia coli	56,151	21-MAR-1997
rx01446	1413	GB_BA2:AE000279	10855	AE000279	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome.	Escherichia coli	56,021	12-Nov-98
		GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.	Streptomyces coelicolor	39,037	04-MAY-1999
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	40,130	17-Jun-98
rx01483	1395	GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	37,752	27-Aug-99
		GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	39,057	17-Jun-98
		GB_BA1:MSG81229CS	30670	L78812	Mycobacterium leprae cosmid B1229 DNA sequence.	Mycobacterium leprae	54,382	15-Jun-96
rx01486	757	GB_BA2:AF027507	5168	AF027507	Mycobacterium smegmatis dGTPase (dgt), and primase (dnaG) genes, complete cds; tRNA-Asn gene, complete sequence.	Mycobacterium smegmatis	52,941	16-Jan-98
		GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	40,941	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,451	22-Aug-97
rx01489	1146	GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	61,194	10-Aug-98
		GB_BA1:CORFADS	1547	D37967	Corynebacterium ammoniagenes gene for FAD synthetase, complete cds	Corynebacterium ammoniagenes	58,021	8-Feb-99
rx01491	774	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,414	22-Aug-97
		GB_BA1:SC10A7	39739	AL078618	Streptomyces coelicolor cosmid 10A7.	Streptomyces coelicolor	36,930	9-Jun-99
		GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,062	17-Jun-98

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TABLE 4: ALIGNMENT RESULTS

rxa01508	1662	GB_EST13:AA356956 GB_OV:OMDNAPROI GB_IN1:CEF28C12 GB_IN1:CEF28C12	255 7327 14653 14653	AA356956 X92380 Z93380 Z93380	EST65614 Jurkat T-cells III Homo sapiens cDNA 5' end, mRNA sequence. O.mossambicus prolactin I gene. Caenorhabditis elegans cosmid F28C12, complete sequence. Caenorhabditis elegans cosmid F28C12, complete sequence.	Homo sapiens Tilapia mossambica Caenorhabditis elegans Caenorhabditis elegans	37,647 38,289 37,984 38,469	21-Apr-97 19-OCT-1995 23-Nov-98 23-Nov-98
rx01512	723	GB_BA1:SCE9 GB_BA1:MAU88875	37730 840	AL049841 U88875	Streptomyces coelicolor cosmid E9. Mycobacterium avium hypoxanthine-guanine phosphoribosyl transferase gene. complete cds.	Streptomyces coelicolor Mycobacterium avium	39,021 57,521	19-MAY-1999 05-MAR-1997
rx01514	711	GB_BA1:MTY15C10 GB_BA1:MTCY7H7B GB_BA1:MLCB2548 GB_PL1:EGGTPCHI GB_PL1:ECOUW93 GB_BA1:ECOUW93 GB_BA1:MTCY49 GB_IN1:DMEZ38847	33050 24244 38916 242 338534 338534 39430 5419	Z95436 Z95557 AL023093 Z49757 U14003 U14003 Z73966 AJ238847	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162. Mycobacterium tuberculosis H37Rv complete genome; segment 153/162. Mycobacterium leprae cosmid B2548. E.gracilis mRNA for GTP cyclohydrolase I (core region). Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes. Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes. Mycobacterium tuberculosis H37Rv complete genome; segment 93/162. Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-Drosophila melanogaster 1).	Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Euglena gracilis Escherichia coli Escherichia coli Mycobacterium tuberculosis Drosophila melanogaster	40,086 43,343 38,177 64,876 38,943 37,500 38,010 36,346	17-Jun-98 18-Jun-98 27-Aug-99 20-OCT-1995 17-Apr-96 17-Apr-96 24-Jun-99 13-Aug-99
rx01516	513	GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR01106 (D1054) RPCI-98 01.1.6 map 55D-55D strain y; on bw sp, *** SEQUENCING IN PROGRESS ***, 86 unordered pieces.	Drosophila melanogaster	37,897	20-Aug-99
rx01517	600	GB_IN2:AF132179 GB_PL2:F6H8 GB_PL2:AF038831	4842 82596 647	AF132179 AF178045 AF038831	Drosophila melanogaster clone LD21677 unknown mRNA. Arabidopsis thaliana BAC F6H8. Sorosporium saponariae internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.	Drosophila melanogaster Arabidopsis thaliana Sorosporium saponariae	36,149 35,846 40,566	3-Jun-99 19-Aug-99 13-Apr-99
rx01528	651	GB_PL2:ATAC005957 GB_BA1:ANANIFBH GB_PR2:AC002461 GB_PR2:AC002461 GB_RO:MM437P9 GB_PR3:AC005740	108355 5936 197273 197273 165901 186780	AC005957 J05111 AC002461 AC002461 AL049866 AC005740	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence. Anabaena sp. (clone AnH20.1) nitrogen fixation operon nifB, fixN, nifS, nifU, and nifH genes, complete cds. Human BAC clone RG204116 from 7q31, complete sequence. Human BAC clone RG204116 from 7q31, complete sequence. Mus musculus chromosome X, clone 437P9. Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Arabidopsis thaliana Anabaena sp. Homo sapiens Homo sapiens Mus musculus Homo sapiens	38,095 38,206 36,623 34,719 37,500 37,031	7-Jan-99 26-Apr-93 20-Aug-97 20-Aug-97 29-Jun-99 01-OCT-1998
rx01551	1998	GB_PR3:AC005740 GB_BA1:MTCY22G10 GB_BA2:ECOUW89 GB_BA1:SCQ11 GB_IN1:CEY62H9A GB_PR4:HSU51003 GB_OM:PIGDAO1 GB_BA1:MTCI125 GB_BA1:U00021 GB_BA1:MLCB1351	186780 35420 176195 15441 47396 3202 395 37432 39193 38936	AC005740 Z84724 U00006 AL096823 AL032630 U51003 M18444 Z98268 U00021 Z95117	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. Mycobacterium tuberculosis H37Rv complete genome; segment 21/162. E. coli chromosomal region from 89.2 to 92.8 minutes. Streptomyces coelicolor cosmid Q11. Caenorhabditis elegans cosmid Y62H9A, complete sequence. Homo sapiens DLX-2 (DLX-2) gene, complete cds. Pig D-amino acid oxidase (DAO) gene, exon 1. Mycobacterium tuberculosis H37Rv complete genome; segment 76/162. Mycobacterium leprae cosmid L247. Mycobacterium leprae cosmid B1351.	Mycobacterium tuberculosis Escherichia coli Streptomyces coelicolor Caenorhabditis elegans Homo sapiens Sus scrofa Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium leprae	38,371 38,064 60,775 38,514 37,730 39,340 63,300 36,756 36,756	17-Jun-98 17-DEC-1993 8-Jul-99 2-Sep-99 07-DEC-1999 27-Apr-93 17-Jun-98 29-Sep-94 24-Jun-97

002227 09994460

**TABLE 4: ALIGNMENT RESULTS**

rx01617	795	GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	40,811	5-Jul-99
		GB_PR2:HS13D10	153147	AL021407	Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.	Homo sapiens	38,768	23-Nov-99
rx01657	723	GB_BA1:MTCY1A10 GB_EST6:D79278	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	39,018	5-Jul-99
		GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	40,656	17-Jun-98
		GB_EST6:D79278	392	D79278	HUM213D06B Human aorta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-213D06 5', mRNA sequence.	Homo sapiens	44,262	9-Feb-96
rx01660	675	GB_BA2:AF129925 GB_BA1:MTV013 GB_RO:MMFV1	10243 11364 6480	AF129925 AL021309 X97719	Thiobacillus ferrooxidans carboxysome operon, complete cds. Mycobacterium tuberculosis H37Rv complete genome; segment 134/162. M. musculus retrovirus restriction gene Fv1.	Thiobacillus ferrooxidans Mycobacterium tuberculosis Mus musculus	40,709 40,986 35,364	17-MAY-1999 17-Jun-98 29-Aug-96
		GB_PAT:A67508	6480	A67508	Sequence 1 from Patent WO9743410.	Mus musculus	35,364	05-MAY-1999
rx01678	651	GB_VI:TVU95309 GB_VI:TVU95303 GB_VI:TVU95302 GB_EST5:H91843	600 600 600 362	U95309 U95303 U95302 H91843	Tula virus O64 nucleocapsid protein gene, partial cds. Tula virus O52 nucleocapsid protein gene, partial cds. Tula virus O24 nucleocapsid protein gene, partial cds. ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb:X63749_rna1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN); mRNA sequence	Tula virus Tula virus Tula virus Homo sapiens	41,894 41,712 39,576 39,157	28-OCT-1997 28-OCT-1997 28-OCT-1997 29-Nov-95
rx01679	1359	GB_ST5:G26925 GB_PL2:AF139451 GB_BA1:SC1C2 GB_EST22:A1064232	362 1202 42210 493	G26925 AF139451 AL031124 A1064232	human STS SHGC-30023, sequence tagged site. Gossypium robinsonii CeiA2 pseudogene, partial sequence. Streptomyces coelicolor cosmid 1C2. GH04563.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence.	Homo sapiens Gossypium robinsonii Streptomyces coelicolor Drosophila melanogaster	39,157 38,910 60,644 38,037	14-Jun-96 1-Jun-99 15-Jan-99 24-Nov-98
rx01692	873	GB_IN2:AF117896 GB_BA2:AF067123	1020 1034	AF117896 AF067123	Drosophila melanogaster neuropeptide F (npf) gene, complete cds. Lactobacillus reuteri cobalamin biosynthesis protein J (cbiJ) gene, partial cds, and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Drosophila melanogaster Lactobacillus reuteri	36,122 48,079	2-Jul-99 3-Jun-98
		GB_RO:RATNFHPEP GB_RO:RSNFH GB_BA2:AF124600	3085 3085 4115	M37227 X13804 AF124600	Rat heavy neurofilament (NF-H) polypeptide, partial cds. Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus. Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Rattus norvegicus Rattus sp. Corynebacterium glutamicum	37,093 37,093 100,000	27-Apr-93 14-Jul-95 04-MAY-1999
rx01698	1353	GB_BA1:MTCY159 GB_BA1:MSGB937CS GB_BA2:AF124600	33818 38914 4115	Z83863 L78820 AF124600	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162. Mycobacterium leprae cosmid B937 DNA sequence. Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Mycobacterium tuberculosis Mycobacterium leprae Corynebacterium glutamicum	36,323 62,780 100,000	17-Jun-98 15-Jun-96 04-MAY-1999
		GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidi) gene, partial cds; polyketide synthase modules 1 through 7 (nida) genes, complete cds; and N-methyltransferase homolog gene, partial cds.	Streptomyces caelestis	40,260	07-DEC-1997
rx01712	805	GB_EST9:C19712 GB_EST21:AA952466	399 278	C19712 AA952466	C19712 Rice panicle at ripening stage Oryza sativa cDNA clone E10821_1A, mRNA sequence. TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence	Oryza sativa Trypanosoma cruzi	45,425 40,876	24-OCT-1996 29-OCT-1998



### TABLE 4: ALIGNMENT RESULTS

TABLE 4. ADDITIONAL INFORMATION									
	GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA	Trypanosoma cruzi	41,367	29-OCT-1998		
				cDNA clone 1404 5', mRNA sequence.					
rxa01719	684			Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN	Homo sapiens	35,651	23-Nov-99		
				PROGRESS ***, in unordered pieces.					
				Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN	Homo sapiens	35,651	23-Nov-99		
				PROGRESS ***, in unordered pieces.					
rxa01720	1332			mq91e08 x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone	Mus musculus	39,671	09-MAR-1999		
				IMAGE:586118 3', mRNA sequence.					
				Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete	Homo sapiens	35,817	18-MAR-1999		
				sequence.					
rxa01746	876			Arabidopsis thaliana BAC TM018A10.	Arabidopsis thaliana	35,698	12-Jul-97		
				Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete	Homo sapiens	37,243	18-MAR-1999		
				sequence.					
				yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone	Homo sapiens	42,812	22-MAY-1995		
rxa01747	1167			IMAGE:36000 3', mRNA sequence.					
				yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone	Homo sapiens	42,655	22-MAY-1995		
				IMAGE:36000 3', mRNA sequence.					
				Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	59,294	17-Jun-98		
rxa01757	924			Mycobacterium leprae cosmid B22.	Mycobacterium leprae	57,584	22-Aug-97		
				Streptomyces coelicolor cosmid 5F7.	Streptomyces coelicolor A3(2)	61,810	22-Jul-99		
				om38c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone	Homo sapiens	39,655	23-Jun-98		
				IMAGE:1543298 3' similar to WP-F28F8.3 CED9757 SMALL NUCLEAR					
rxa01807	915			RIBONUCLEOPROTEIN E.; mRNA sequence.					
				EST110563 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone	Rattus sp.	35,942	2-Apr-98		
				RPNB181 5' end, mRNA sequence.					
				NCP6G8T7 Perithecial Neurospora crassa cDNA clone NP6G8 3' end, mRNA	Neurospora crassa	40,000	12-Apr-98		
rxa01807	915			sequence.					
				Aeropyrum pernix genomic DNA, section 6/7.	Aeropyrum pernix	40,067	22-Jun-99		
				Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN	Drosophila melanogaster	35,450	16-OCT-1999		
				PROGRESS ***, 75 unordered pieces.					
rxa01821	401			Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN	Drosophila melanogaster	35,450	16-OCT-1999		
				PROGRESS ***, 75 unordered pieces.					
				Corynebacterium glutamicum 3' ppc gene, secG gene, ood gene	Corynebacterium glutamicum	100,000	7-Jan-99		
				and 5' soxA gene.					
rxa01835	654			Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7.	Rattus norvegicus	38,692	15-DEC-1994		
				Anas platyrhynchos (Super M) IgY upislon heavy chain gene, exon 2.	Anas platyrhynchos	36,962	15-Feb-99		
				486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays	Zea mays	38,109	26-Apr-99		
				cDNA, mRNA sequence.					
rxa01835	654			SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	37,021	26-MAR-1999		
				RPC11-4112, TV RPC1-11 Homo sapiens genomic clone RPC1-11-4112,	Homo sapiens	37,021	8-Apr-99		
				genomic survey sequence.					

## TAB. E 4: ALIGNMENT RESULTS

rxa01850	1470	GB_BA2:ECOUW67_0 GB_BA2:AE000392 GB_BA2:U32715 GB_HTG1:CEY64F11	110000 10345 13136 177748	U18997 AE000392 U32715 Z99776	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes. Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome. Haemophilus influenzae Rd section 30 of 163 of the complete genome. Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS *** in unordered pieces.	37,196 38,021 39,860 37,564	Escherichia coli Escherichia coli Haemophilus influenzae Rd Caenorhabditis elegans	U18997 12-Nov-98 29-MAY-1998 14-OCT-1998
rxa01878	1002	GB_HTG1:CEY64F11  GB_HTG1:CEY64F11 GB_HTG1:CEY64F11	  177748 177748	  Z99776 Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS *** in unordered pieces. Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS *** in unordered pieces.	37,564  37,576	Caenorhabditis elegans Caenorhabditis elegans	14-OCT-1998  14-OCT-1998
rxa01892	852	GB_BA1:MTCY274 GB_BA1:MLCB250 GB_BA1:MSGB1529CS	39991 40603 36985	Z74024 Z97369 L78824	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. Mycobacterium leprae cosmid B250. Mycobacterium leprae cosmid B1529 DNA sequence.	35,910 64,260 64,260	Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium leprae	19-Jun-98 27-Aug-99 15-Jun-96
rxa01894	978	GB_BA1:MTCY274 GB_IN1:CELF46H5 GB_HTG3:AC009204	39991 38886 115633	Z74024 U41543 AC009204	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. Caenorhabditis elegans cosmid F46H5. Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***. 94 unordered pieces.	37,229 38,525 31,579	Mycobacterium tuberculosis Caenorhabditis elegans Drosophila melanogaster	19-Jun-98 29-Nov-96 18-Aug-99
rxa01920	1125	GB_BA2:AF112536  GB_BA1:CANRDFGEN	1798  6054	AF112536  Y09572	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds. Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	99,733  70,321	Corynebacterium glutamicum  Corynebacterium ammoniagenes	5-Aug-99  18-Apr-98
rxa01928	960	GB_BA2:AF050168  GB_BA1:CGPAN GB_PL1:AP000423	1228  2164 154478	AF050168  X96580 AP000423	Corynebacterium ammoniagenes ribonucleoside diphosphate reductase small subunit (nrdF) gene, complete cds. C.glutamicum panB, panC & xylB genes. Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	100,000 35,917  33,925	Corynebacterium glutamicum ammoniagenes Corynebacterium glutamicum Chloroplast Arabidopsis thaliana Chloroplast Arabidopsis thaliana	11-MAY-1999 15-Sep-99  15-Sep-99
rxa01929	936	GB_PL1:AP000423  GB_BA1:CGPAN GB_BA1:XCU33548	154478  2164 8429	AP000423  X96580 U33548	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia. C.glutamicum panB, panC & xylB genes. Xanthomonas campestris hrpB pathogenicity locus proteins HrpB1, HrpB2, HrpB3, HrpB4, HrpB5, HrpB6, HrpB7, HrpB8, HrpA1, and ORF62 genes, complete cds.	100,000 38,749  39,305 61,417	Corynebacterium glutamicum Xanthomonas campestris pv. vesicatoria  Xanthomonas campestris Crithidia fasciculata	11-MAY-1999 19-Sep-96  14-Sep-93 18-Jun-96
rxa01940	1059	GB_BA1:XANHRPB6A GB_IN2:CFU43371  GB_BA2:AE001467 GB_RO:AF175967 GB_BA1:CGDAPE GB_BA1:CGDNAAROP	1329 1060  11601 3492 1966 2612	M99174 U43371  AE001467 AF175967 X81379 X85965	Xanthomonas campestris hrpB6 gene, complete cds. Crithidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds. Helicobacter pylori, strain J99 section 28 of 132 of the complete genome. Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds. C.glutamicum dapE gene and orf2. C.glutamicum ORF3 and aroP gene.	39,305 61,417  38,560 40,275 100,000 38,889	Xanthomonas campestris Crithidia fasciculata  Helicobacter pylori J99 Mus musculus Corynebacterium glutamicum Corynebacterium glutamicum	14-Sep-93 18-Jun-96  20-Jan-99 26-Sep-99 8-Aug-95 30-Nov-97
rxa02022	1230	GB_BA1:CGDNAAROP	2612	X85965	C.glutamicum ORF3 and aroP gene.	36,647	Anabaena PCC7120	17-Feb-96
rxa02024	859	GB_BA1:APU47055  GB_BA1:MTIC364	6469  29540	U47055  Z93777	Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hesA genes, partial cds. Mycobacterium tuberculosis H37Rv complete genome, segment 52/162.	59,415	Mycobacterium tuberculosis	17-Jun-98

### **TABLE 4: ALIGNMENT RESULTS**

TABLE 4: ALIGNMENT REFERENCES							
	GB_BA1:MSGB1912CS	38503	L01536	M. leprae genomic dna sequence, cosmid b1912.	Mycobacterium leprae	57,093	14-Jun-96
	GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	57,210	09-MAR-1995
rx02027							
rx02031							
rx02072	1464	2037	X72855	C.glutamicum GDHA gene.	Corynebacterium glutamicum	99,317	24-MAY-1993
	GB_BA1:CGGDHA	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	94,367	30-Jul-99
	GB_BA1:CGGDH	2037	Y18494	Pseudomonas aeruginosa ghA gene, strain PAC1.	Pseudomonas aeruginosa	62,247	6-Feb-99
	GB_BA1:PAE18494	1628	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	38,442	17-Jun-98
rx02085	2358	22550	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	56,486	24-Jun-97
	GB_BA1:MLCB33	42224	M87049	E. coli genomic sequence of the region from 84.5 to 86.5 minutes.	Escherichia coli	52,127	29-MAY-1995
	GB_BA1:ECOUW85	91414	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE.782737 5', Homo sapiens mRNA sequence.	Homo sapiens	34,163	4-Jun-97
rx02093	927	444	AA641937	ns18b10.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1183963 5', Homo sapiens mRNA sequence.	Homo sapiens	35,586	27-OCT-1997
	GB_EST17:AA641937	444	AC003074	Human PAC clone DJ0596009 from 7p15, complete sequence.	Homo sapiens	31,917	6-Nov-97
	GB_PR3:AC003074	143029	AL023496	Streptomyces coelicolor cosmid 1A6.	Streptomyces coelicolor	35,818	13-Jan-99
rx02106	1179	37620	AL023496	Streptomyces coelicolor cosmid 1A6.	Streptomyces coelicolor	34,274	31-DEC-1998
	GB_BA1:SC1A6	179651	AC005553	Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.	Homo sapiens	41,162	18-MAY-1995
	GB_PR4:AC005553	397	R49746	yg71g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38768 5' similar to gb:V00567 BETA-2-MICROGLOBULIN	Homo sapiens		
	GB_EST3:R49746			PRECURSOR (HUMAN);. mRNA sequence.			
rx02111	1407	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
	GB_BA1:SC6G10	41171	U00010	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
	GB_BA1:U00010	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
	GB_BA1:MTCY336	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98	Drosophila melanogaster	37,909	24-Sep-99
rx02112	960			09.D.8 map 96F-96F strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***			
	GB_HTG3:AC010579			121 unordered pieces.			
	GB_GSS3:B09839	1191	B09839	T12A12-Sp6 TAMU Arabidopsis thaliana genomic clone T12A12, genomic survey sequence.	Arabidopsis thaliana	37,843	14-MAY-1997
	GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98	Drosophila melanogaster	37,909	24-Sep-99
	GB_BA1:SCSECYDNA	6154	X83011	09.D.8 map 96F-96F strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***			
	GB_EST32:AI731596	568	AI731596	121 unordered pieces.	Streptomyces coelicolor	36,533	02-MAR-1998
rx02134	1044			S.coelicolor secY locus DNA.			
	GB_BA1:SCSECYDNA	6154	X83011	BNLGH10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]. mRNA sequence.	Gossypium hirsutum	33,451	11-Jun-99
	GB_EST32:AI731596			S.coelicolor secY locus DNA.	Streptomyces coelicolor	36,756	02-MAR-1998

**TABLE 4: ALIGNMENT RESULTS**

rx02135	1197	GB_PR3:HS525L6	168111	AL023807	Human DNA sequence from clone RP3-525L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG island, complete sequence.	Homo sapiens	34,365	23-Nov-99
		GB_PL2:ATF21P8	85785	AL022347	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project)	Arabidopsis thaliana	34,325	9-Jun-99
rx02136	645	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	33,874	26-Jun-98
		GB_PL2:ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
		GB_PL2:F15K9	71097	AC005278	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
rx02139	1962	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	34,281	26-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,904	17-Jun-98
		GB_BA1:MSG81554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
		GB_BA1:MSG81551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
rx02153	903	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,104	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	99,224	2-Jul-97
		GB_BA1:CGARGCJBD	4355	X86157	C glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02154	414	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds	Corynebacterium glutamicum	98,551	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	98,477	2-Jul-97
		GB_BA1:CGARGCJBD	4355	X86157	C glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02155	1287	GB_BA1:CGARGCJBD	4355	X86157	C glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,767	25-Jul-96
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,378	1-Jul-98
		GB_BA1:MSG81133CS	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-96

**TABLE 4: ALIGNMENT RESULTS**

rx02156	1074	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA1:CGARGCJBD	4355	X86157		Corynebacterium glutamicum	100,000	25-Jul-96
		GB_BA2:AE001816	10007	AE001816	Thermotoga maritima section 128 of 136 of the complete genome.	Thermotoga maritima	50,238	2-Jun-99
rx02157	1296	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,612	1-Jul-98
		GB_BA1:CGARGCJBD	4355	X86157		Corynebacterium glutamicum	99,612	25-Jul-96
		GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	57,278	17-Jun-98
rx02158	1080	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA2:AF031518	2045	AF031518		Corynebacterium glutamicum	99,898	5-Jan-99
		GB_BA1:CGARGCJBD	4355	X86157		Corynebacterium glutamicum	100,000	25-Jul-96
rx02159	636	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
		GB_BA2:AF031518	2045	AF031518		Corynebacterium glutamicum	88,679	5-Jan-99
		GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
rx02160	1326	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum argininosuccinate synthetase (argG) gene, complete cds.	Corynebacterium glutamicum	99,774	1-Jul-98
		GB_BA2:AF030520	1206	AF030520		Corynebacterium glutamicum	99,834	19-Nov-97
		GB_BA1:SCARGGH	1909	Z49111	S.clavuligerus argG gene and argH gene (partial).	Streptomyces clavuligerus	65,913	22-Apr-96

**TABLE 4: ALIGNMENT RESULTS**

rx02162	1554	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	88,524	1-Jul-98
		GB_BA2:AF048764	1437	AF048764	Corynebacterium glutamicum argininosuccinate lyase (argH) gene, complete cds.	Corynebacterium glutamicum	87,561	1-Jul-98
rx02176	1251	GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	64,732	17-Jun-98
		GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	36,998	17-Jun-98
		GB_BA1:CGGLTG	3013	X66112	C glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	39,910	17-Feb-95
rx02189	861	GB_PL2:PGU65399	2700	U65399	Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.	basidiomycete CECT 20197	38,474	19-Jul-97
		GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	35,941	16-Sep-98
		GB_BA1:MSG81970CS	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	40,286	15-Jun-96
rx02193	1701	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	33,689	16-Sep-98
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	99,353	6-Feb-99
		GB_PAT:E04307	1581	E04307	DNA encoding Brevibacterium flavum aspartase.	Corynebacterium glutamicum	99,367	29-Sep-97
rx02194	966	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,651	17-Apr-96
		GB_BA2:AF050166	840	AF050166	Corynebacterium glutamicum ATP phosphoribosyltransferase (hisG) gene, complete cds.	Corynebacterium glutamicum	98,214	5-Jan-99
rx02195	393	GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	93,805	6-Feb-99
		GB_PAT:E08649	188	E08649	DNA encoding part of aspartase from coryneform bacteria.	Corynebacterium glutamicum	100,000	29-Sep-97
		GB_BA2:AF086704	264	AF086704	Corynebacterium glutamicum phosphoribosyl-ATP-pyrophosphohydrolase (hisE) gene, complete cds	Corynebacterium glutamicum	100,000	8-Feb-99
rx02197	551	GB_STS:G01195	332	G01195	Eubacterium acidaminophilum grdR, grdI, grdH genes and partial ldc, grdT genes.	Eubacterium acidaminophilum	39,075	5-Aug-98
		GB_BA1:MTCY261	27322	Z97559	fruit fly STS Dm1930 clone DS06959 T7.	Drosophila melanogaster	35,542	28-Feb-95
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	33,938	17-Jun-98
rx02198	2599	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,517	27-Aug-99
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	36,770	01-MAR-1994
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	38,674	01-MAR-1994
rx02208	1025	GB_BA1:MTCY261	27322	Z97559	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,465	27-Aug-99
		GB_BA1:U00017	42157	U00017	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	37,577	17-Jun-98
		GB_BA1:AP000063	185300	AP000063	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	59,823	01-MAR-1994
rx02229	948	GB_PR4:AC006236	127593	AC006236	Aeropyrum pernix genomic DNA, section 67.	Mycobacterium leprae	39,442	22-Jun-99
		GB_BA1:MSGY154	40221	AD000002	Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	53,541	03-DEC-1996
rx02234	3462	GB_BA1:U00019	36033	U00019	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	40,407	17-Jun-98
		GB_BA1:MSG837CS	38914	L78820	Mycobacterium leprae cosmid B2235.	Mycobacterium tuberculosis	40,541	01-MAR-1994
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	66,027	15-Jun-96
		GB_BA2:U01072	4393	U01072	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	71,723	18-Jun-98
					Mycobacterium bovis BCG orotidine-5'-monophosphate decarboxylase (uraA) gene.	Mycobacterium bovis	67,101	22-DEC-1993

**TABLE 4: ALIGNMENT RESULTS**

rx02235	727	GB_BA1:MSU91572	960	U91572	Mycobacterium smegmatis carbamoyl phosphate synthetase (pyrAB) gene, partial cds and orotidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds.	Mycobacterium smegmatis	60,870	22-MAR-1997
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
rx02237	693	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,844	23-Jun-98
		GB_BA2:AF077324	5228	AF077324	Rhodococcus equi strain 103 plasmid RE-VP1 fragment f.	Rhodococcus equi	41,185	5-Nov-98
		GB_EST2:AU017763	586	AU017763	AU017763 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J074A04 3', mRNA sequence.	Mus musculus	38,616	19-OCT-1998
rx02239	1389	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	56,282	23-Jun-98
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
rx02240	1344	EM_PAT:E09855	1239	E09855	gDNA encoding S-adenosylmethionine synthetase.	Corynebacterium glutamicum	99,515	07-OCT-1997 (Rel. 52, Created)
		GB_PAT:A37831	5392	A37831	Sequence 1 from Patent WO9408014.	Streptomyces pristinaespiralis	63,568	05-MAR-1997
rx02246	1107	GB_BA2:AF117274	2303	AF117274	Streptomyces spectabilis flavoprotein homolog Dfp (dfp) gene, partial cds, and S-adenosylmethionine synthetase (metK) gene, complete cds.	Streptomyces spectabilis	65,000	31-MAR-1999
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	52,909	29-Sep-97
rx02247	756	GB_PAT:132742	5589	132742	Sequence 1 from patent US 55893355.	Unknown.	52,909	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 55893355.	Unknown.	57,937	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	57,937	03-OCT-1997 (Rel. 52, Created)
rx02248	1389	GB_PAT:132742	5589	132742	Sequence 1 from patent US 55893355.	Unknown.	57,937	6-Feb-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 55893355	Unknown.	61,843	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	61,843	03-OCT-1997 (Rel. 52, Created)
rx02249	600	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	61,843	29-Sep-97
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	64,346	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 55893355.	Unknown.	64,346	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 55893355.	Unknown.	64,346	6-Feb-97

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**TABLE 4: ALIGNMENT RESULTS**

rx02250	643	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	56,318	29-Sep-97
		GB_PAT:I32742	5589	I32742	Sequence 1 from patent US 55893355.	Unknown.	56,318	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	56,318	03-OCT-1997 (Rel. 52, Created)
rx02262	1269	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE	2028	X93513	C-glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
rx02263	488	GB_VI:HEHCMVCG	229354	X17403	Human cytomegalovirus strain AD169 complete genome.	human herpesvirus 5	38,651	10-Feb-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	37,526	7-Jan-99
rx02272	1368	EM_PAT:E09373	1591	E09373	Creatinine deiminase gene.	Bacillus sp.	96,928	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:D38505	1591	D38505	Bacillus sp. gene for creatinine deaminase, complete cds.	Bacillus sp.	96,781	7-Aug-98
		GB_HTG2:AC006595	146070	AC006595	Homo sapiens, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	36,264	20-Feb-99
rx02281	1545	GB_GSS12:AQ411010	551	AQ411010	HS_2257_B1_H02_MR CIT Approved Human Genomic Sperm Library D	Homo sapiens	36,197	17-MAR-1999
					Homo sapiens genomic clone Plate=2257 Col=3 Row=P, genomic survey sequence.			
		GB_EST23:A1128623	363	A1128623	qa62c01.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691328 3', mRNA sequence.	Homo sapiens	37,017	05-OCT-1998
		GB_PL2.ATAC007019	102335	AC007019	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence.	Arabidopsis thaliana	33,988	16-MAR-1999
rx02299	531	GB_BA2:AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds.	Corynebacterium glutamicum	100,000	02-MAY-1999
		GB_GSS9:AQ164310	507	AQ164310	HS_2171_A2_E01_MR CIT Approved Human Genomic Sperm Library D	Homo sapiens	37,278	16-OCT-1998
					Homo sapiens genomic clone Plate=2171 Col=2 Row=I, genomic survey sequence.			
rx02311	813	GB_VI:MH68TKH	4557	X93468	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	40,288	3-Sep-96
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98	Drosophila melanogaster	36,454	27-OCT-1999
					48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces			
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98	Drosophila melanogaster	36,454	27-OCT-1999
					48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.			



### TABLE 4: ALIGNMENT RESULTS

	GB_BA2:RRU65510	16259	U65510	Rhodospirillum rubrum CO-induced hydrogenase operon (cooM, cooK, cooL, cooX, cooJ, cooH) genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds.	Rhodospirillum rubrum	37,828	9-Apr-97	
rxa02315	1752	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	49,418	03-DEC-1996	
		40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	49,360	17-Jun-98	
		40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	38,150	03-DEC-1996	
	402	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999	
		111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999	
		89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	36,181	06-OCT-1999	
	rxa02319	1080	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	37,792	03-DEC-1996
			40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	37,792	17-Jun-98
		476	A1117213	ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5' mRNA sequence.	Mus musculus	35,084	2-Sep-98	
1320		2582	X91189	B.ammoniaenes purK and purE genes.	Corynebacterium ammoniagenes	61,731	14-Jan-97	
rxa02350	618	2582	X91189	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,624	10-Feb-99	
		42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,847	10-Feb-99	
		2582	X91189	B.ammoniaenes purK and purE genes.	Corynebacterium ammoniagenes	64,286	14-Jan-97	
	rxa02373	1038	129528	X94335	S.cerevisiae 130kb DNA fragment from chromosome XV.	Saccharomyces cerevisiae	36,617	15-Jul-97
		50984	X90518	S.cerevisiae DNA of 51 Kb from chromosome XV right arm.	Saccharomyces cerevisiae	36,617	1-Nov-95	
		1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	56,123	29-Sep-97	
		1853	I06030	Sequence 4 from Patent EP 0305608.	Unknown.	56,220	02-DEC-1993	
rxa02375	1350	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	56,220	21-MAY-1993	
		3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	99,332	2-Aug-96	
rxa02380	777	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99	
		169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99	
		41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	38,088	17-Jun-98	
		120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999	
		120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999	

**TABLE 4: ALIGNMENT RESULTS**

rx02382	1419	GB_BA1:CGPROAGEN	1783	X82929	C.glutamicum proA gene.	Corynebacterium glutamicum	98,802	23-Jan-97
		GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	38,054	17-Jun-98
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Ogb protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	98,529	2-Aug-96
rx02400	693	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_PAT:186191	2135	I86191	Sequence 3 from patent US 5700661.	Unknown.	100,000	10-Jun-98
		GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	100,000	26-Sep-95
rx02432	1098	GB_GSS15:AQ606842	574	AQ606842	HS_5404_B2_E07_TTA RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence.	Homo sapiens	39,716	10-Jun-99
		GB_EST1:T05804	406	T05804	EST03693 Fetal brain, Stragelene (cat#36206) Homo sapiens cDNA clone HFBG363 similar to EST containing Alu repeat, mRNA sequence.	Homo sapiens	37,915	30-Jun-93
		GB_PL1:AB006699	77363	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence.	Arabidopsis thaliana	35,526	20-Nov-99
rx02458	1413	GB_BA2:AF114233	1852	AF114233	Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds	Corynebacterium glutamicum	100,000	7-Feb-99
		GB_EST37:AW013061	578	AW013061	ODT-0033 Winter flounder ovary Pleuronectes americanus cDNA clone ODT-0033 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER), mRNA sequence.	Pleuronectes americanus	39,175	10-Sep-99
		GB_GSS15:AQ650027	728	AQ650027	Sheared DNA-5L2, TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-5L2, genomic survey sequence.	Trypanosoma brucei	39,281	22-Jun-99
rx02469	1554	GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	39,634	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	59,343	27-Aug-99
		GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	48,899	17-Sep-98
rx02497	1050	GB_BA2:CGU31224	422	U31224	Corynebacterium glutamicum (ppx) gene, partial cds.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	59,429	17-Jun-98
		GB_BA1:SCE7	16911	AL049819	Streptomyces coelicolor cosmid E7.	Streptomyces coelicolor	39,510	10-MAY-1999
rx02499	933	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoeductase (proC) gene, complete cds.	Corynebacterium glutamicum	97,749	2-Aug-96
		GB_BA1:NG17PILA	1920	X13965	Neisseria gonorrhoeae pilA gene.	Neisseria gonorrhoeae	43,249	30-Sep-93
		GB_HTG2:AC007984	129715	AC007984	Drosophila melanogaster chromosome 3 clone BACR05C10 (D781) RPCI-98 05.C.10 map 97D-97E strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 87 unordered pieces.	Drosophila melanogaster	33,406	2-Aug-99
rx02501	1188	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	39,357	17-Jun-98
		GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	51,768	01-MAR-1994
		GB_VI:HE1CG	152261	X14112	Herpes simplex virus (HSV) type 1 complete genome.	human herpesvirus 1	39,378	17-Apr-97
rx02503	522	GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	39,922	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	39,922	3-Sep-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	34,911	28-Jul-98
rx02504	681	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	54,940	17-Jun-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	41,265	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	41,265	3-Sep-98
rx02516	1386	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,723	04-DEC-1998

**TABLE 4: ALIGNMENT RESULTS**

rx02517	570	GB_BA1:U00013 GB_BA1:MTV007 GB_BA1:MLCL536 GB_BA1:U00013 GB_BA1:SCC22 GB_OV:AF137219 GB_EST30:A1645057	35881 32806 36224 35881 22115 831 301	U00013 AL021184 Z99125 U00013 AL096839 AF137219 A1645057	Mycobacterium leprae cosmid B1496. Mycobacterium tuberculosis H37Rv complete genome; segment 64/162. Mycobacterium leprae cosmid L536. Mycobacterium leprae cosmid B1496. Streptomyces coelicolor cosmid C22. Amia calva mixed lineage leukemia-like protein (MIL) gene, partial cds. vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence	Mycobacterium leprae Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium leprae Streptomyces coelicolor Amia calva Mus musculus	37,723 61,335 37,018 37,018 37,071 36,853 41,860	01-MAR-1994 17-Jun-98 04-DEC-1998 01-MAR-1994 12-Jul-99 7-Sep-99 29-Apr-99
rx02532	1170	GB_EST20:AA822595 GB_HTG2:AF130866 GB_HTG2:AF130866 GB_PL1:ATT12J5	429 118874 118874 84499	AA822595 AF130866 AF130866 AL035522	vs52a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence. Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS *** in unordered pieces. Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS *** in unordered pieces. Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAIL project).	Mus musculus Homo sapiens Homo sapiens Arabidopsis thaliana	42,353 40,754 40,754 35,063	17-Feb-98 21-MAR-1999 21-MAR-1999 24-Feb-99
rx02550	1434	GB_BA1:MTCY279 GB_BA1:MSGB1970CS GB_BA2:SC2H4	9150 39399 25970	Z97991 L78815 AL031514	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162. Mycobacterium leprae cosmid B1970 DNA sequence. Streptomyces coelicolor cosmid 2H4.	Mycobacterium tuberculosis Mycobacterium leprae Streptomyces coelicolor A3(2)	37,773 39,024 37,906	17-Jun-98 15-Jun-96 19-OCT-1999
rx02559	1026	GB_BA1:MTV004 GB_PAT:I28684 GB_BA1:MTU27357	69350 5100 5100	AL009198 I28684 U27357	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162. Sequence 1 from patent US 5573915. Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	Mycobacterium tuberculosis Unknown. Mycobacterium tuberculosis	47,358 39,138 39,138	18-Jun-98 6-Feb-97 26-Sep-95
rx02622	1683	GB_BA2:AE001780 GB_OV:AF064564 GB_OV:AF064564	11997 49254 49254	AE001780 AF064564 AF064564	Thermotoga maritima section 92 of 136 of the complete genome. Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds. Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Thermotoga maritima Fugu rubripes Fugu rubripes	44,914 39,732 36,703	2-Jun-99 17-Aug-99 17-Aug-99
rx02623	714	GB_GSS5:AQ818728 GB_HTG5:AC011083 GB_GSS6:AQ826948 GB_VI:BRSMGP GB_VI:BRSMGP	444 198586 544 462 462	AQ818728 AC011083 AQ826948 M86652 M86652	HS_5268_A1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence. Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces. HS_5014_A2_C12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence. Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds. Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Homo sapiens Homo sapiens Homo sapiens Bovine respiratory syncytial virus Bovine respiratory syncytial virus	38,801 35,714 39,146 37,013 37,013	26-Aug-99 19-Nov-99 27-Aug-99 28-Apr-93 28-Apr-93

002227" 09994460

**TABLE 4: ALIGNMENT RESULTS**

rx02645	1953	GB_PAT:A45577 GB_PAT:A45581 GB_BA1:CORILVA	1925 1925 1925	A45577 A45581 L01508	Sequence 1 from Patent WO9519442. Sequence 5 from Patent WO9519442. Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum	39,130 39,130 39,130	07-MAR-1997 07-MAR-1997 26-Apr-93
rx02646	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	99,138	26-Apr-93
rx02648	1326	GB_PAT:A45585 GB_PAT:A45583 GB_OV:ICTCNC GB_EST11:AA265464	1925 1925 2049 345	A45585 A45583 M83111 AA265464	Sequence 9 from Patent WO9519442. Sequence 7 from Patent WO9519442. Ictalurus punctatus cyclic nucleotide-gated channel RNA sequence. mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5' mRNA sequence.	Corynebacterium glutamicum Corynebacterium glutamicum Ictalurus punctatus Mus musculus	99,066 99,066 38,402 38,665	07-MAR-1997 07-MAR-1997 24-MAY-1993 20-MAR-1997
rx02653		GB_GSS8:AQ006950	480	AQ006950	CIT-HSP-2294E14, TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.	Homo sapiens	36,074	27-Jun-98
rx02687	1068	GB_BA1:CORPHEA GB_PAT:E04483 GB_PAT:E06110 GB_PL1:HVC4H GB_PR2:HS310H5	1088 948 948 59748 29718	M13774 E04483 E06110 Y14573 Z69705	C.glutamicum pheA gene encoding prephenate dehydratase, complete cds. DNA encoding prephenate dehydratase. DNA encoding prephenate dehydratase. Hordeum vulgare DNA for chromosome 4H. Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island.	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum Hordeum vulgare Homo sapiens	99,715 98,523 98,523 36,593 36,089	26-Apr-93 29-Sep-97 29-Sep-97 25-MAR-1999 22-Nov-99
rx02754	1461	GB_PR3:AC004754 GB_HTG2:AC008223	39188 130212	AC004754 AC008223	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence. Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.L18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Homo sapiens Drosophila melanogaster	36,089 32,757	28-MAY-1998 2-Aug-99
rx02758	1422	GB_HTG2:AC008223 GB_BA1:MTCY71 GB_HTG5:AC011678 GB_HTG5:AC011678 GB_BA2:AF064070	130212 42729 171967 171967 23183	AC008223 Z92771 AC011678 AC011678 AF064070	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.L18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces. Mycobacterium tuberculosis H37Rv complete genome; segment 141/162. Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS***, 20 unordered pieces. Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS***, 20 unordered pieces. Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphatase (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds; and putative galactosyl transferase gene, partial cds.	Drosophila melanogaster Mycobacterium tuberculosis Homo sapiens Homo sapiens Burkholderia pseudomallei	32,757 37,838 35,331 33,807 36,929	2-Aug-99 10-Feb-99 5-Nov-99 5-Nov-99 20-Jan-99

TABLE 4: ALIGNMENT RESULTS

rx02771	678	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcIAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,852	14-Sep-98
		GB_IN1:CELT19B4	37121	U80438	Caenorhabditis elegans cosmid T19B4.	Caenorhabditis elegans	43,836	04-DEC-1996
		GB_EST36:AV193572	360	AV193572	AV193572 Yuji Kohara unpublished cDNA: Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence.	Caenorhabditis elegans	48,588	22-Jul-99
rx02772	1158	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcIAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,914	14-Sep-98
		GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	38,339	17-Jun-98
		GB_BA1:U00011	40429	U00011	Mycobacterium leprae cosmid B1177.	Mycobacterium leprae	38,996	01-MAR-1994
rx02790	1266	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	37,640	17-Jun-98
		GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC11-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,906	3-Jun-99
		GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC11-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,280	3-Jun-99
rx02791	951	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,765	17-Jun-98
		GB_OV:CHKCEK2	3694	M35195	Chicken tyrosine kinase (cek2) mRNA, complete cds.	Gallus gallus	38,937	28-Apr-93
		GB_BA1:MSASDASK	5037	Z17372	M.smegmatis asd, ask-alpha, and ask-beta genes.	Mycobacterium smegmatis	38,495	9-Aug-94
rx02802	1194	GB_EST24:AI223401	169	AI223401	qq48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ;, mRNA sequence.	Homo sapiens	40,828	27-OCT-1998
		GB_EST24:AI223401	169	AI223401	qq48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ;, mRNA sequence.	Homo sapiens	40,828	27-OCT-1998
rx02814	494	GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	58,418	17-Jun-98
		GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	40,496	17-Jun-98
		GB_PR1:HSAJ2962	778	AJ002962	Homo sapiens mRNA for hB-FABP.	Homo sapiens	39,826	8-Jan-98
rx02843	608	GB_BA1:CGAJ4934	1160	AJ004934	Corynebacterium glutamicum dapD gene, complete CDS.	Corynebacterium glutamicum	100,000	17-Jun-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	37,710	17-Jun-98
		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	39,626	09-MAR-1995
rxs03205	963	GB_BA1:BLSIGBGN	2906	Z49824	Blactofermentum orf1 gene and sigB gene.	Corynebacterium glutamicum	98,854	25-Apr-96
		GB_EST21:AA980237	377	AA980237	IMAGE:1348414.5' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN. ;, mRNA sequence.	Mus musculus	41,489	27-MAY-1998
		GB_EST23:AI158316	371	AI158316	ud27c05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1447112.5', mRNA sequence.	Mus musculus	38,005	30-Sep-98
rxs03223	1237	GB_IN1:LMFL2743	38368	AL031910	Leishmania major Friedlin chromosome 4 cosmid L2743.	Leishmania major	39,869	15-DEC-1999
		GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,930	17-DEC-1999

TABLE 4: ALIGNMENT RESULTS

GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,634	17-DEC-1999
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